F1 cont'd

important role in intracellular signal transmission through this "YxxM" structure. Furthermore, it has been reported that CTLA-4 also has a sequence represented by "YxxM," namely "YVKM (Tyr-Val-Lys-Met)" (SEQ ID NO:20) in its cytoplasmic region and that, after being stimulated, SYP associates with this sequence.

Replace the paragraph beginning at page 34, line 3, with the following rewritten paragraph:

F2

To determine percent homology between two sequences, the algorithm of Karlin and Altschul (1990) Proc. Natl. Acad. Sci. USA 87:2264-2268, modified as in Karlin and Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-5877 is used. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST nucleotide searches are performed with the NBLAST program, score = 100, word length = 12 to obtain nucleotide sequences homologous to a nucleic acid molecules of the invention. BLAST protein searches are performed with the XBLAST program, score = 50, word length = 3 to obtain amino acid sequences homologous to a VRK1 or VRK2 protein molecules. To obtain gapped alignments for comparison purposes, Gapped BLAST is utilized as described in Altschul et al. (1997) Nucleic Acids Res. 25:3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) are used. See, web site of National Center for Biotechnology Information (NCBI), which is a division of National Library of Medicine (NLM) at the National Institute of Health (NIH) in USA.

Replace the paragraph beginning at page 84, line 4, with the following rewritten paragraph:

F3

After the purified "JTT-1antigen" was subjected to SDS-PAGE, the N-terminal amino acid sequence was determined by the usual method. The result revealed that "JTT-1 antigen" contained an amino acid sequence Glu-Leu-Asn-Asp-Leu-Ala-Asn-His-Arg (amino acid residues 21-29 of SEQ ID NO:13).

Replace the paragraph beginning at page 88, line 15, with the following rewritten paragraph:

F4

The nucleotide sequence of clone "T132A7" was determined by dideoxy method with "Auto Read Sequencing Kit" (Pharmacia) and "A.L.F. DNA Sequencer" (Pharmacia). In addition, the deduced amino acid sequence of "rat JTT-1 antigen" encoded by the nucleotide sequence was analyzed with gene analysis software "GENEWORKS" (IntelliGenetics). The nucleotide sequence and the deduced amino acid sequence are shown in SEQ ID NO:4 and SEQ ID NO:13, respectively.

Replace the paragraph beginning at page 94, line 10, with the following rewritten paragraph:

F5

The nucleotide sequence of each of the five clones was determined by dideoxy method with "Auto Read Sequencing Kit" (Pharmacia) and "A.L.F. DNA Sequencer" (Pharmacia). Four of the five clones comprise the same nucleotide sequence. The nucleotide sequence of cDNA encoding the full length of "mouse JTT-1 antigen" and the deduced amino acid sequence are shown in SEQ ID NO:5 and SEQ ID NO:14, respectively.

Replace the paragraph beginning at page 97, line 22, with the following rewritten paragraph:

F6

The nucleotide sequences of the two clones were determined by the dideoxy method with "Auto Read Sequencing Kit" (Pharmacia) and A.L.F. DNA Sequencer (Pharmacia). The two clones comprise the same nucleotide sequence. The nucleotide sequence of cDNA encoding the full length of the obtained "rat JTT-1 antigen" and the deduced amino acid sequence are shown in SEQ ID NO:6 and SEQ ID NO:15, respectively. The amino acid sequence (SEQ ID NO:6 or SEQ ID NO:15) deduced from the obtained cDNA sequence was compared with the amino acid sequence (SEQ ID NO:4 or SEQ ID NO:13) deduced from the obtained cDNA sequence encoding "rat JTT-1 antigen" cloned in Example 7 (Figure 14). As shown in Figure 14,

the amino acid sequence encoded by the cDNA cloned in this test was completely the same as that encoded by the cDNA encoding "rat JTT-1 antigen" obtained in Example 7, except that (1) C-terminal three continuous amino acid residues (Met-Thr-Ser) changes into Thr-Ala-Pro, and (2) subsequent to the Thr-Ala-Pro, 16 continuous amino acid residues (Leu-Arg-Ala-Leu-Gly-Arg-Gly-Glu-His-Ser-Ser-Cys-Gln-Asp-Arg-Asn) (SEQ ID NO:24) are added. This indicates that the cDNA cloned in this test encodes an alternative splicing variant of "rat JTT-1 antigen" obtained in Example 7.

F6 cont'd

Replace the paragraph beginning at page 105, line 21, with the following rewritten paragraph:

-- In order to amplify the cDNA encoding the extracellular region of "rat JTT-1 antigen" by PCR, a 5' primer having an XhoI restriction site (5'-CTGCTCGAGATGAAGCCCTACTTCTCG-3', SEQ ID NO:7) and 3' primer having BamHI restriction site (5'-ACCCTACGGGTAACGGATCCTTCAGCTGGCAA-3', SEQ ID NO:8) at their termini were designed and synthesized. Using cDNA clone "T132A7" obtained in Example 7 encoding the full length of "rat JTT-1 antigen" as a template, PCR was performed with the primers to prepare a cDNA comprising the cDNA encoding the extracellular region of "rat JTT-1 antigen" having XhoI and BamHI restriction sites at its ends. The PCR products so obtained were digested with XhoI and BamHI and separated by agarose gel electrophoresis to isolate an about 450-bp band predicted to be the cDNA fragment encoding a desired extracellular region. The isolated cDNA fragment was subcloned into pBluescript II SK (+) (Stratagene) cleaved with XhoI and BamHI. Sequence analysis with an automated fluorescence DNA sequencer (Applied Biosystems) revealed that the cDNA fragment comprises the region encoding an amino acid sequence corresponding to amino acid residues 1 to 141 of "rat JTT-1 antigen" (SEQ ID NO:4 or SEQ ID NO:13). --

F7

In the claims:

Cancel claims 1 to 36.

Add new claims 37 to 214.